

21703N

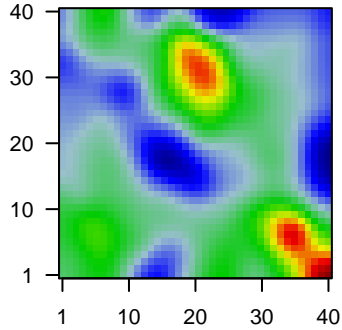
Global Summary

%DE = 0.05
 # genes with fdr < 0.2 = 1560 (1040 + / 520 -)
 # genes with fdr < 0.1 = 1084 (747 + / 337 -)
 # genes with fdr < 0.05 = 749 (533 + / 216 -)
 # genes with fdr < 0.01 = 454 (336 + / 118 -)

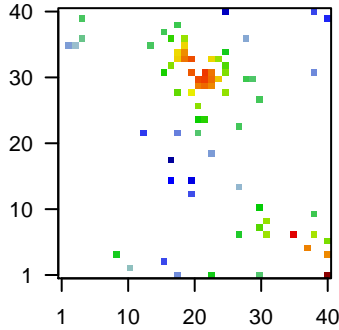
 # genes in genesets = 16360

<FC> = 0
 <t-score> = 0.17
 <p-value> = 0.26
 <fdr> = 0.95

Portrait



Top 100 DE genes



Global Genelist

Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
1	1556573_s_at	1.73	2e-16	30 x 1 novel transcript
2	201123_s_at	-1.96	2e-16	11 x 2 eukaryotic translation initiation factor 5A [Source:HGNC Symbol;Acc:HGNC:10000]
3	201909_at	1.18	2e-16	18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:10000]
4	204103_at	1.68	2e-16	22 x 30 C-C motif chemokine ligand 4 [Source:HGNC Symbol;Acc:HGNC:10000]
5	205067_at	1.62	2e-16	22 x 30 interleukin 1 beta [Source:HGNC Symbol;Acc:HGNC:5992]
6	205114_s_at	1.27	2e-16	23 x 30 C-C motif chemokine ligand 3 [Source:HGNC Symbol;Acc:HGNC:10000]
7	206115_at	1.09	2e-16	37 x 5 early growth response 3 [Source:HGNC Symbol;Acc:HGNC:10000]
8	206373_at	-0.88	2e-16	17 x 15 Zic family member 1 [Source:HGNC Symbol;Acc:HGNC:1287]
9	206918_s_at	-1.43	2e-16	13 x 22 copine 1 [Source:HGNC Symbol;Acc:HGNC:2314]
10	206932_at	1.22	2e-16	23 x 30 cholesterol 25-hydroxylase [Source:HGNC Symbol;Acc:HGNC:10000]
11	207659_s_at	1.02	2e-16	35 x 7 myelin-associated oligodendrocyte basic protein [Source:HGNC Symbol;Acc:HGNC:10000]
12	207978_s_at	2.12	2e-16	9 x 4 nuclear receptor subfamily 4 group A member 3 [Source:HGNC Symbol;Acc:HGNC:10000]
13	209959_at	1.6	2e-16	21 x 29 nuclear receptor subfamily 4 group A member 3 [Source:HGNC Symbol;Acc:HGNC:10000]
14	210118_s_at	1.63	2e-16	22 x 29 interleukin 1 alpha [Source:HGNC Symbol;Acc:HGNC:5991]
15	212657_s_at	1.84	2e-16	16 x 31 interleukin 1 receptor antagonist [Source:HGNC Symbol;Acc:HGNC:10000]
16	212845_at	0.79	2e-16	30 x 27 sterile alpha motif domain containing 4A [Source:HGNC Symbol;Acc:HGNC:10000]
17	214038_at	2.02	2e-16	23 x 31 C-C motif chemokine ligand 8 [Source:HGNC Symbol;Acc:HGNC:10000]
18	216979_at	1.85	2e-16	14 x 35 nuclear receptor subfamily 4 group A member 3 [Source:HGNC Symbol;Acc:HGNC:10000]
19	221371_at	1.65	2e-16	29 x 30 TNF superfamily member 18 [Source:HGNC Symbol;Acc:HGNC:10000]
20	227404_s_at	0.89	2e-16	18 x 28

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	10.77	NULL	17	BP antigen processing and presentation of peptide or polysaccharide antigen fragments
2	9.23	NULL	18	BP eosinophil chemotaxis
3	8.9	NULL	388	BP immune response
4	8.4	NULL	4278	BP plasma membrane
5	7.93	NULL	26	BP lymphocyte chemotaxis
6	7.79	NULL	36	BP monocyte chemotaxis
7	7.78	NULL	43	BP antigen processing and presentation
8	7.76	NULL	364	BP inflammatory response
9	7.39	NULL	7387	BP membrane
10	7.15	NULL	289	BP cytokine-mediated signaling pathway
11	6.97	NULL	88	BP cellular response to interferon-gamma
12	6.81	NULL	207	BP cytokine activity
13	6.76	NULL	236	BP chemical synaptic transmission
14	6.36	NULL	574	BP synapse
15	6.08	NULL	74	BP neutrophil chemotaxis
16	5.94	NULL	72	BP positive regulation of inflammatory response
17	5.93	NULL	59	BP positive regulation of T cell proliferation
18	5.81	NULL	43	BP chemokine activity
19	5.6	NULL	12	BP negative regulation by host of viral transcription
20	5.46	NULL	627	BP ion transport
<i>Underexpressed</i>				
1	-5.52	NULL	630	BP cell cycle
2	-5.2	NULL	158	BP DNA replication
3	-4.66	NULL	229	BP mRNA splicing, via spliceosome
4	-4.5	NULL	1387	BP regulation of transcription, DNA-templated
5	-4.36	NULL	97	BP DNA recombination
6	-4.33	NULL	1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
7	-4.18	NULL	394	BP cell division
8	-3.96	NULL	366	BP DNA repair
9	-3.7	NULL	1145	BP regulation of transcription by RNA polymerase II
10	-3.67	NULL	342	BP chromatin organization
11	-3.55	NULL	56	BP mRNA 3'-end processing
12	-3.53	NULL	484	BP cellular response to DNA damage stimulus
13	-3.51	NULL	11	BP glycerophospholipid biosynthetic process
14	-3.5	NULL	16	BP negative regulation of growth
15	-3.44	NULL	80	BP retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum
16	-3.39	NULL	10	BP positive regulation of tumor necrosis factor-mediated signaling pathway
17	-3.14	NULL	85	BP chromosome segregation
18	-3.12	NULL	11	BP exit from mitosis
19	-3.11	NULL	20	BP signal transduction involved in regulation of gene expression
20	-3.1	NULL	17	BP positive regulation of cellular protein metabolic process

p-values

